



SEQUENCE LISTING

<110> Ward, Larry D.
Thomson, Helen

<120> Poxvirus vector encoding retrovirus (eg HIV) and cytokine

<130> 19746

<140> 10/575,928
<141> 2006-14-14

<150> AU 2003905642
<151> 2003-10-15

<150> AU 2003905683
<151> 2003-10-16

<160> 7

<170> PatentIn version 3.2

<210> 1
<211> 1329
<212> DNA
<213> Human immunodeficiency virus

<220>
<221> CDS
<222> (1)..(1329)

<400> 1

atg ggt gcg aga gcg tcg gta tta agc ggg gga gaa tta gat aaa tgg	48
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp	
1 5 10 15	
gaa aaa att cgg tta agg cca ggg gga aag aaa aaa tat aag tta aaa	96
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys	
20 25 30	
cat ata gta tgg gca agc agg gag cta gaa cga ttc gca gtc aat cct	144
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro	
35 40 45	
ggc ctg tta gaa aca tca gaa ggc tgc aga caa ata ttg gga cag cta	192
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu	
50 55 60	
cag cca tcc ctt cag aca gga tca gaa gaa ctt aga tca tta tat aat	240
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn	
65 70 75 80	
aca gta gca acc ctc tat tgt gta cat caa agg ata gat gta aaa gac	288
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp	
85 90 95	
acc aag gaa gct tta gag aag ata gag gaa gag caa aac aaa agt aag	336
Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys	
100 105 110	
aaa aag gca cag caa gca gca gct gca gct ggc aca gga aac agc agc	384
Lys Lys Ala Gln Gln Ala Ala Ala Ala Gly Thr Gly Asn Ser Ser	
115 120 125	

cag Gln 130	gtc Val	agc Ser	caa Gln	aat Asn	tac Tyr	cct Pro 135	ata Ile	gtg Val	cag Gln	aac Asn	cta Leu 140	cag Gln	ggg Gly	caa Gln	atg Met	432
gta Val 145	cat His	cag Gln	gcc Ala	ata Ile	tca Ser 150	cct Pro	aga Arg	act Thr	tta Leu	aat Asn 155	gca Ala	tgg Trp	gta Val	aaa Lys	gta Val 160	480
gta Val	gaa Glu	gaa Glu	aag Lys	gct Ala 165	ttc Phe	agc Ser	cca Pro	gaa Glu	gta Val 170	ata Ile	ccc Pro	atg Met	ttt Phe	tca Ser 175	gca Ala	528
tta Leu	tca Ser	gaa Glu	gga Gly 180	gcc Ala	acc Thr	cca Pro	caa Gln	gat Asp 185	tta Leu	aac Asn	acc Thr	atg Met	cta Leu 190	aac Asn	aca Thr	576
gtg Val	ggg Gly	gga Gly	cat His	caa Gln	gca Ala	gcc Ala	atg Met 200	caa Gln	atg Met	tta Leu	aaa Lys	gag Glu 205	act Thr	atc Ile	aat Asn	624
gag Glu	gaa Glu 210	gct Ala	gca Ala	gaa Glu	tgg Trp	gat Asp 215	aga Arg	gtg Val	cat His	cca Pro	gtg Val 220	cat His	gca Ala	ggg Gly	cct Pro	672
att Ile 225	gca Ala	cca Pro	ggc Gly	caa Gln	atg Met 230	aga Arg	gaa Glu	cca Pro	agg Arg	gga Gly 235	agt Ser	gac Asp	ata Ile	gca Ala	gga Gly 240	720
act Thr	act Thr	agt Ser	acc Thr	ctt Leu 245	cag Gln	gaa Glu	caa Gln	ata Ile	gga Gly 250	tgg Trp	atg Met	aca Thr	aat Asn	aat Asn 255	cca Pro	768
cct Pro	atc Ile	cca Pro	gta Val 260	gga Gly	gaa Glu	atc Ile	tat Tyr	aaa Lys 265	aga Arg	tgg Trp	ata Ile	atc Ile	ctg Leu 270	gga Gly	tta Leu	816
aat Asn	aaa Lys	ata Ile 275	gta Val	aga Arg	atg Met	tat Tyr	agc Ser 280	cct Pro	acc Thr	agc Ser	att Ile 285	ctg Leu	gac Asp	ata Ile	aga Arg	864
caa Gln	gga Gly 290	cca Pro	aag Lys	gaa Glu	ccc Pro	ttt Phe 295	aga Arg	gat Asp	tat Tyr	gta Val	gac Asp 300	cgg Arg	ttc Phe	tat Tyr	aaa Lys	912
act Thr 305	cta Leu	aga Arg	gcc Ala	gaa Glu	caa Gln 310	gct Ala	tca Ser	cag Gln	gat Asp	gta Val 315	aaa Lys	aat Asn	tgg Trp	atg Met	aca Thr 320	960
gaa Glu	acc Thr	ttg Leu	ttg Leu	gtc Val 325	caa Gln	aat Asn	gca Ala	aac Asn	cca Pro 330	gat Asp	tgt Cys	aag Lys	act Thr	att Ile 335	tta Leu	1008
aaa Lys	gca Ala	ttg Leu	gga Gly 340	cca Pro	gca Ala	gct Ala	aca Thr	cta Leu 345	gaa Glu	gaa Glu	atg Met	atg Met	aca Thr 350	gca Ala	tgt Cys	1056
cag Gln	gga Gly	gtg Val 355	ggg Gly	gga Gly	ccc Pro	ggc Gly	cat His 360	aaa Lys	gca Ala	aga Arg	gtt Val 365	ttg Leu	gct Ala	gaa Glu	gcc Ala	1104
atg Met	agc Ser 370	caa Gln	gta Val	aca Thr	aat Asn	cca Pro 375	gct Ala	aac Asn	ata Ile	atg Met	atg Met 380	cag Gln	aga Arg	ggc Gly	aat Asn	1152

ttt agg aac caa aga aag act gtt aag tgt ttc aat tgt ggc aaa gaa 1200
Phe Arg Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu
385 390 395 400

ggg cac ata gcc aaa aat tgc agg gcc cct agg aaa aag ggc tgt tgg 1248
Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp
405 410 415

aga tgt gga agg gaa gga cac caa atg aaa gat tgc act gag aga cag 1296
Arg Cys Gly Arg Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln
420 425 430

gct aat ttt tta ggg aag atc tgg cct tcc tac 1329
Ala Asn Phe Leu Gly Lys Ile Trp Pro Ser Tyr
435 440

<210> 2
<211> 443
<212> PRT
<213> Human immunodeficiency virus

<400> 2

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp
85 90 95

Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Ala Ala Gly Thr Gly Asn Ser Ser
115 120 125

Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met
130 135 140

Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
145 150 155 160

Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
 165 170 175
 Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
 180 185 190
 Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn
 195 200 205
 Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro
 210 215 220
 Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly
 225 230 235 240
 Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro
 245 250 255
 Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu
 260 265 270
 Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg
 275 280 285
 Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
 290 295 300
 Thr Leu Arg Ala Glu Gln Ala Ser Gln Asp Val Lys Asn Trp Met Thr
 305 310 315 320
 Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu
 325 330 335
 Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys
 340 345 350
 Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala
 355 360 365
 Met Ser Gln Val Thr Asn Pro Ala Asn Ile Met Met Gln Arg Gly Asn
 370 375 380
 Phe Arg Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu
 385 390 395 400
 Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp
 405 410 415

Arg Cys Gly Arg Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln
 420 425 430

Ala Asn Phe Leu Gly Lys Ile Trp Pro Ser Tyr
 435 440

<210> 3
 <211> 3012
 <212> DNA
 <213> Human immunodeficiency virus

<220>
 <221> CDS
 <222> (1)..(3012)

<400> 3
 ttt ttt agg gaa gat ctg gcc ttc cta caa ggg aag gcc agg gaa ttt 48
 Phe Phe Arg Glu Asp Leu Ala Phe Leu Gln Gly Lys Ala Arg Glu Phe
 1 5 10 15
 tct tca gag cag acc aga gcc aac agc ccc acc aga aga gag ctt cag 96
 Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln
 20 25 30
 gtt tgg gga gga gaa aac aac tcc ctc tca gaa gca gga gcc gat aga 144
 Val Trp Gly Gly Glu Asn Asn Ser Leu Ser Glu Ala Gly Ala Asp Arg
 35 40 45
 caa gga act gta tcc ttt aac ttc cct cag atc act ctt tgg caa cga 192
 Gln Gly Thr Val Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg
 50 55 60
 ccc ctc gtc aca ata agg ata ggg ggg caa cta aag gaa gct cta tta 240
 Pro Leu Val Thr Ile Arg Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu
 65 70 75 80
 gat aca gga gca gat gat aca gta tta gaa gaa atg aat ttg cca gga 288
 Asp Thr Gly Ala Asp Asp Thr Val Leu Glu Glu Met Asn Leu Pro Gly
 85 90 95
 aaa tgg aaa cca aaa atg ata ggg gga att gga ggt ttt atc aaa gta 336
 Lys Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val
 100 105 110
 aga cag tac gat cag ata cct gta gaa atc tgt gga cat aaa gct ata 384
 Arg Gln Tyr Asp Gln Ile Pro Val Glu Ile Cys Gly His Lys Ala Ile
 115 120 125
 ggt aca gta tta gta gga cct aca cct gtc aac ata att gga aga aat 432
 Gly Thr Val Leu Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn
 130 135 140
 ctg ttg act cag att ggt tgt act tta aat ttc ccc att agt cct att 480
 Leu Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe Pro Ile Ser Pro Ile
 145 150 155 160
 gaa act gta cca gta aaa tta aag cca gga atg gat ggc cca aaa gtt 528
 Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val
 165 170 175
 aag caa tgg cca ttg aca gaa gaa aaa ata aaa gca tta gta gag ata 576
 5

Lys	Gln	Trp	Pro 180	Leu	Thr	Glu	Glu	Lys 185	Ile	Lys	Ala	Leu	Val 190	Glu	Ile		
tgt	aca	gaa	atg	gaa	aag	gaa	ggg	aaa	att	tca	aaa	att	ggg	cct	gaa	624	
Cys	Thr	Glu 195	Met	Glu	Lys	Glu	Gly 200	Lys	Ile	Ser	Lys	Ile 205	Gly	Pro	Glu		
aat	cca	tac	aat	act	cca	gta	ttt	gct	ata	aag	aaa	aaa	gac	agt	act	672	
Asn	Pro 210	Tyr	Asn	Thr	Pro	Val 215	Phe	Ala	Ile	Lys	Lys 220	Lys	Asp	Ser	Thr		
aaa	tgg	aga	aaa	cta	gta	gat	ttc	aga	gaa	ctt	aat	aaa	aga	act	caa	720	
Lys 225	Trp	Arg	Lys	Leu	Val 230	Asp	Phe	Arg	Glu	Leu 235	Asn	Lys	Arg	Thr	Gln 240		
gac	ttc	tgg	gaa	gtt	cag	tta	gga	ata	cca	cac	ccc	gca	ggg	tta	aaa	768	
Asp	Phe	Trp	Glu	Val 245	Gln	Leu	Gly	Ile	Pro 250	His	Pro	Ala	Gly	Leu 255	Lys		
aag	aaa	aaa	tca	gta	aca	gta	ttg	gat	gtg	ggt	gat	gca	tac	ttt	tca	816	
Lys	Lys	Lys	Ser 260	Val	Thr	Val	Leu	Asp 265	Val	Gly	Asp	Ala	Tyr 270	Phe	Ser		
gtt	ccc	tta	gat	aaa	gac	ttt	aga	aag	tat	act	gca	ttt	acc	ata	cct	864	
Val	Pro	Leu 275	Asp	Lys	Asp	Phe	Arg 280	Lys	Tyr	Thr	Ala	Phe 285	Thr	Ile	Pro		
agt	ata	aac	aat	gag	aca	cca	ggg	att	aga	tat	cag	tac	aat	gtg	ctg	912	
Ser	Ile 290	Asn	Asn	Glu	Thr	Pro 295	Gly	Ile	Arg	Tyr	Gln 300	Tyr	Asn	Val	Leu		
cca	cag	gga	tgg	aaa	gga	tca	cca	gca	ata	ttc	caa	agt	agc	atg	aca	960	
Pro 305	Gln	Gly	Trp	Lys	Gly 310	Ser	Pro	Ala	Ile	Phe 315	Gln	Ser	Ser	Met	Thr 320		
aaa	atc	tta	gag	cct	ttt	aga	aaa	cag	aat	cca	gac	ata	gtt	atc	tat	1008	
Lys	Ile	Leu	Glu	Pro 325	Phe	Arg	Lys	Gln	Asn 330	Pro	Asp	Ile	Val 335	Ile	Tyr		
caa	tac	atg	gat	gat	ttg	tat	gta	gga	tct	gac	tta	gaa	ata	ggg	cag	1056	
Gln	Tyr	Met	Asp 340	Asp	Leu	Tyr	Val	Gly 345	Ser	Asp	Leu	Glu	Ile 350	Gly	Gln		
cat	aga	aca	aaa	ata	gag	gaa	ctg	aga	cag	cat	ctg	ttg	agg	tgg	gga	1104	
His	Arg	Thr 355	Lys	Ile	Glu	Glu	Leu 360	Arg	Gln	His	Leu	Arg 365	Arg	Trp	Gly		
ttt	acc	aca	cca	gac	aaa	aaa	cat	cag	aaa	gaa	cct	cca	ttc	ctt	tgg	1152	
Phe	Thr 370	Thr	Pro	Asp	Lys	Lys 375	His	Gln	Lys	Glu	Pro 380	Pro	Phe	Leu	Trp		
atg	ggt	tat	gaa	ctc	cat	cct	gat	aaa	tgg	aca	gta	cag	cct	ata	atg	1200	
Met 385	Gly	Tyr	Glu	Leu	His 390	Pro	Asp	Lys	Trp	Thr	Val	Gln	Pro	Ile	Met 400		
ctg	cca	gaa	aaa	gac	agc	tgg	act	gtc	aat	gac	ata	cag	aag	tta	gtg	1248	
Leu	Pro	Glu	Lys	Asp 405	Ser	Trp	Thr	Val	Asn 410	Asp	Ile	Gln	Lys	Leu 415	Val		
gga	aaa	ttg	aat	tgg	gca	agt	cag	att	tat	gca	ggg	att	aaa	gta	aag	1296	
Gly	Lys	Leu	Asn 420	Trp	Ala	Ser	Gln	Ile 425	Tyr	Ala	Gly	Ile 430	Lys	Val	Lys		
cag	tta	tgt	aaa	ctc	ctt	aga	gga	acc	aaa	gca	cta	aca	gaa	gta	ata	1344	

Gln	Leu	Cys 435	Lys	Leu	Leu	Arg	Gly 440	Thr	Lys	Ala	Leu	Thr 445	Glu	Val	Ile	
cca	cta	aca	gaa	gaa	gca	gag	cta	gaa	ctg	gca	gaa	aac	agg	gag	att	1392
Pro	Leu	Thr 450	Glu	Glu	Ala	Glu 455	Leu	Glu	Leu	Ala	Glu 460	Asn	Arg	Glu	Ile	
cta	aaa	gaa	cca	gta	cat	gaa	gta	tat	tat	gac	cca	tca	aaa	gac	tta	1440
Leu	Lys	Glu	Pro	Val	His 470	Glu	Val	Tyr	Tyr	Asp 475	Pro	Ser	Lys	Asp	Leu 480	
gta	gca	gaa	ata	cag	aag	cag	ggg	caa	ggc	caa	tgg	aca	tat	caa	att	1488
Val	Ala	Glu	Ile	Gln 485	Lys	Gln	Gly	Gln	Gly 490	Gln	Trp	Thr	Tyr	Gln 495	Ile	
tat	caa	gag	cca	ttt	aaa	aat	ctg	aaa	aca	gga	aag	tat	gca	agg	atg	1536
Tyr	Gln	Glu	Pro 500	Phe	Lys	Asn	Leu	Lys 505	Thr	Gly	Lys	Tyr	Ala 510	Arg	Met	
agg	ggt	gcc	cac	act	aat	gat	gta	aaa	cag	tta	aca	gag	gca	gtg	caa	1584
Arg	Gly	Ala 515	His	Thr	Asn	Asp	Val 520	Lys	Gln	Leu	Thr	Glu 525	Ala	Val	Gln	
aaa	gta	tcc	aca	gaa	agc	ata	gta	ata	tgg	gga	aag	att	cct	aaa	ttt	1632
Lys	Val 530	Ser	Thr	Glu	Ser	Ile 535	Val	Ile	Trp	Gly	Lys 540	Ile	Pro	Lys	Phe	
aaa	cta	ccc	ata	caa	aag	gaa	aca	tgg	gaa	gca	tgg	tgg	atg	gag	tat	1680
Lys 545	Leu	Pro	Ile	Gln	Lys 550	Glu	Thr	Trp	Glu	Ala 555	Trp	Trp	Met	Glu	Tyr 560	
tgg	caa	gct	acc	tgg	att	cct	gag	tgg	gag	ttt	gtc	aat	acc	cct	ccc	1728
Trp	Gln	Ala	Thr	Trp 565	Ile	Pro	Glu	Trp	Glu 570	Phe	Val	Asn	Thr	Pro 575	Pro	
tta	gtg	aaa	tta	tgg	tac	cag	tta	gag	aaa	gaa	ccc	ata	gta	gga	gca	1776
Leu	Val	Lys	Leu 580	Trp	Tyr	Gln	Leu	Glu 585	Lys	Glu	Pro	Ile	Val 590	Gly	Ala	
gaa	act	ttc	tat	gta	gat	ggg	gca	gct	aat	agg	gag	act	aaa	tta	gga	1824
Glu	Thr	Phe 595	Tyr	Val	Asp	Gly	Ala 600	Ala	Asn	Arg	Glu	Thr 605	Lys	Leu	Gly	
aaa	gca	gga	tat	gtt	act	gac	aga	gga	aga	caa	aaa	gtt	gtc	tcc	ata	1872
Lys	Ala 610	Gly	Tyr	Val	Thr	Asp 615	Arg	Gly	Arg	Gln	Lys 620	Val	Val	Ser	Ile	
gct	gac	aca	aca	aat	cag	aag	act	gaa	tta	caa	gca	att	cat	cta	gct	1920
Ala 625	Asp	Thr	Thr	Asn	Gln 630	Lys	Thr	Glu	Leu	Gln 635	Ala	Ile	His	Leu	Ala 640	
ttg	cag	gat	tcg	gga	tta	gaa	gta	aac	ata	gta	aca	gac	tca	caa	tat	1968
Leu	Gln	Asp	Ser	Gly 645	Leu	Glu	Val	Asn	Ile 650	Val	Thr	Asp	Ser	Gln 655	Tyr	
gca	tta	gga	atc	att	caa	gca	caa	cca	gat	aag	agt	gaa	tca	gag	tta	2016
Ala	Leu	Gly 660	Ile	Ile	Gln	Ala	Gln	Pro 665	Asp	Lys	Ser	Glu	Ser 670	Glu	Leu	
gtc	agt	caa	ata	ata	gag	cag	tta	ata	aaa	aag	gaa	aag	gtc	tac	ctg	2064
Val	Ser	Gln 675	Ile	Ile	Glu	Gln	Leu 680	Ile	Lys	Lys	Glu	Lys 685	Val	Tyr	Leu	
gca	tgg	gta	cca	gca	cac	aaa	gga	att	gga	gga	aat	gaa	caa	gta	gat	2112

Ala	Trp	Val	Pro	Ala	His	Lys	Gly	Ile	Gly	Gly	Asn	Glu	Gln	Val	Asp	
690						695					700					
aaa	tta	gtc	agt	gct	gga	atc	agg	aaa	gta	cta	ttt	ttg	aat	gga	ata	2160
Lys	Leu	Val	Ser	Ala	Gly	Ile	Arg	Lys	Val	Leu	Phe	Leu	Asn	Gly	Ile	
705					710					715					720	
gat	aag	gcc	caa	gaa	gaa	cat	gag	aaa	tat	cac	agt	aat	tgg	aga	gca	2208
Asp	Lys	Ala	Gln	Glu	Glu	His	Glu	Lys	Tyr	His	Ser	Asn	Trp	Arg	Ala	
				725					730					735		
atg	gct	agt	gat	ttt	aac	ctg	cca	cct	gta	gta	gca	aaa	gaa	ata	gta	2256
Met	Ala	Ser	Asp	Phe	Asn	Leu	Pro	Pro	Val	Val	Ala	Lys	Glu	Ile	Val	
			740					745					750			
gcc	agc	tgt	gat	aaa	tgt	cag	cta	aaa	gga	gaa	gcc	atg	cat	gga	caa	2304
Ala	Ser	Cys	Asp	Lys	Cys	Gln	Leu	Lys	Gly	Glu	Ala	Met	His	Gly	Gln	
		755					760					765				
gta	gac	tgt	agt	cca	gga	ata	tgg	caa	cta	gat	tgt	aca	cat	cta	gaa	2352
Val	Asp	Cys	Ser	Pro	Gly	Ile	Trp	Gln	Leu	Asp	Cys	Thr	His	Leu	Glu	
	770					775					780					
gga	aaa	att	atc	ctg	gta	gca	gtt	cat	gta	gcc	agt	gga	tat	ata	gaa	2400
Gly	Lys	Ile	Ile	Leu	Val	Ala	Val	His	Val	Ala	Ser	Gly	Tyr	Ile	Glu	
785					790					795					800	
gca	gaa	gtt	att	cca	gca	gag	aca	ggg	cag	gaa	aca	gca	tat	ttt	ctc	2448
Ala	Glu	Val	Ile	Pro	Ala	Glu	Thr	Gly	Gln	Glu	Thr	Ala	Tyr	Phe	Leu	
				805					810					815		
tta	aaa	tta	gca	gga	aga	tgg	cca	gta	aaa	aca	ata	cat	aca	gac	aat	2496
Leu	Lys	Leu	Ala	Gly	Arg	Trp	Pro	Val	Lys	Thr	Ile	His	Thr	Asp	Asn	
			820					825					830			
ggc	agc	aat	ttc	acc	agt	act	acg	gtt	aag	gcc	gcc	tgt	tgg	tgg	gca	2544
Gly	Ser	Asn	Phe	Thr	Ser	Thr	Thr	Val	Lys	Ala	Ala	Cys	Trp	Trp	Ala	
		835					840					845				
ggg	atc	aag	cag	gaa	ttt	ggc	att	ccc	tac	aat	ccc	caa	agt	caa	gga	2592
Gly	Ile	Lys	Gln	Glu	Phe	Gly	Ile	Pro	Tyr	Asn	Pro	Gln	Ser	Gln	Gly	
	850					855					860					
gta	gta	gaa	tct	atg	aat	aat	gaa	tta	aag	aaa	att	ata	gga	cag	gta	2640
Val	Val	Glu	Ser	Met	Asn	Asn	Glu	Leu	Lys	Lys	Ile	Ile	Gly	Gln	Val	
865					870					875					880	
aga	gat	cag	gct	gaa	cac	ctt	aag	aca	gca	gta	caa	atg	gca	gta	ttc	2688
Arg	Asp	Gln	Ala	Glu	His	Leu	Lys	Thr	Ala	Val	Gln	Met	Ala	Val	Phe	
				885					890					895		
atc	cac	aat	ttt	aaa	aga	aaa	ggg	ggg	att	ggg	gga	tac	agt	gca	ggg	2736
Ile	His	Asn	Phe	Lys	Arg	Lys	Gly	Gly	Ile	Gly	Gly	Tyr	Ser	Ala	Gly	
			900					905					910			
gaa	aga	ata	gta	gac	ata	ata	gca	aca	gac	ata	caa	act	aaa	gaa	cta	2784
Glu	Arg	Ile	Val	Asp	Ile	Ile	Ala	Thr	Asp	Ile	Gln	Thr	Lys	Glu	Leu	
		915					920					925				
caa	aag	caa	att	aca	aaa	att	caa	aat	ttt	cgg	gtt	tat	tac	agg	gac	2832
Gln	Lys	Gln	Ile	Thr	Lys	Ile	Gln	Asn	Phe	Arg	Val	Tyr	Tyr	Arg	Asp	
	930					935					940					
aac	aaa	gat	ccc	ctt	tgg	aaa	gga	cca	gca	aag	ctt	ctc	tgg	aaa	ggc	2880

Asn	Lys	Asp	Pro	Leu	Trp	Lys	Gly	Pro	Ala	Lys	Leu	Leu	Trp	Lys	Gly		
945					950					955					960		
gaa	ggg	gca	gta	gta	ata	caa	gat	aat	agt	gac	ata	aaa	gta	gtg	cca	2928	
Glu	Gly	Ala	Val	Val	Ile	Gln	Asp	Asn	Ser	Asp	Ile	Lys	Val	Val	Pro		
				965					970					975			
aga	aga	aaa	gca	aaa	atc	att	agg	gat	tat	gga	aaa	cag	atg	gca	ggc	2976	
Arg	Arg	Lys	Ala	Lys	Ile	Ile	Arg	Asp	Tyr	Gly	Lys	Gln	Met	Ala	Gly		
			980					985					990				
gat	gat	tgt	gtg	gca	agt	aga	cag	gat	gag	gat	tag					3012	
Asp	Asp	Cys	Val	Ala	Ser	Arg	Gln	Asp	Glu	Asp							
		995					1000										

<210> 4
 <211> 1003
 <212> PRT
 <213> Human immunodeficiency virus
 <400> 4

Phe	Phe	Arg	Glu	Asp	Leu	Ala	Phe	Leu	Gln	Gly	Lys	Ala	Arg	Glu	Phe		
1				5					10					15			
Ser	Ser	Glu	Gln	Thr	Arg	Ala	Asn	Ser	Pro	Thr	Arg	Arg	Glu	Leu	Gln		
		20						25					30				
Val	Trp	Gly	Gly	Glu	Asn	Asn	Ser	Leu	Ser	Glu	Ala	Gly	Ala	Asp	Arg		
		35					40					45					
Gln	Gly	Thr	Val	Ser	Phe	Asn	Phe	Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg		
	50					55				60							
Pro	Leu	Val	Thr	Ile	Arg	Ile	Gly	Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu		
65					70				75						80		
Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly		
			85						90					95			
Lys	Trp	Lys	Pro	Lys	Met	Ile	Gly	Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val		
			100					105					110				
Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Val	Glu	Ile	Cys	Gly	His	Lys	Ala	Ile		
		115					120					125					
Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn		
	130					135					140						
Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile		
145					150					155					160		
Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	Pro	Gly	Met	Asp	Gly	Pro	Lys	Val		

165

170

175

Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile
 180 185 190

Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu
 195 200 205

Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr
 210 215 220

Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln
 225 230 235 240

Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys
 245 250 255

Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser
 260 265 270

Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro
 275 280 285

Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu
 290 295 300

Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr
 305 310 315 320

Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr
 325 330 335

Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln
 340 345 350

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
 355 360 365

Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
 370 375 380

Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Met
 385 390 395 400

Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val
 405 410 415

Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys Val Lys
 10

420					425					430					
Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala	Leu	Thr	Glu	Val	Ile
		435					440					445			
Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala	Glu	Asn	Arg	Glu	Ile
	450					455					460				
Leu	Lys	Glu	Pro	Val	His	Glu	Val	Tyr	Tyr	Asp	Pro	Ser	Lys	Asp	Leu
465					470					475					480
Val	Ala	Glu	Ile	Gln	Lys	Gln	Gly	Gln	Gly	Gln	Trp	Thr	Tyr	Gln	Ile
				485					490					495	
Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu	Lys	Thr	Gly	Lys	Tyr	Ala	Arg	Met
			500					505					510		
Arg	Gly	Ala	His	Thr	Asn	Asp	Val	Lys	Gln	Leu	Thr	Glu	Ala	Val	Gln
		515					520					525			
Lys	Val	Ser	Thr	Glu	Ser	Ile	Val	Ile	Trp	Gly	Lys	Ile	Pro	Lys	Phe
	530					535					540				
Lys	Leu	Pro	Ile	Gln	Lys	Glu	Thr	Trp	Glu	Ala	Trp	Trp	Met	Glu	Tyr
545					550					555					560
Trp	Gln	Ala	Thr	Trp	Ile	Pro	Glu	Trp	Glu	Phe	Val	Asn	Thr	Pro	Pro
				565					570					575	
Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu	Lys	Glu	Pro	Ile	Val	Gly	Ala
			580					585					590		
Glu	Thr	Phe	Tyr	Val	Asp	Gly	Ala	Ala	Asn	Arg	Glu	Thr	Lys	Leu	Gly
		595					600					605			
Lys	Ala	Gly	Tyr	Val	Thr	Asp	Arg	Gly	Arg	Gln	Lys	Val	Val	Ser	Ile
	610					615					620				
Ala	Asp	Thr	Thr	Asn	Gln	Lys	Thr	Glu	Leu	Gln	Ala	Ile	His	Leu	Ala
625					630					635					640
Leu	Gln	Asp	Ser	Gly	Leu	Glu	Val	Asn	Ile	Val	Thr	Asp	Ser	Gln	Tyr
				645					650					655	
Ala	Leu	Gly	Ile	Ile	Gln	Ala	Gln	Pro	Asp	Lys	Ser	Glu	Ser	Glu	Leu
			660					665					670		
Val	Ser	Gln	Ile	Ile	Glu	Gln	Leu	Ile	Lys	Lys	Glu	Lys	Val	Tyr	Leu

675

680

685

Ala Trp Val Pro Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp
690 695 700

Lys Leu Val Ser Ala Gly Ile Arg Lys Val Leu Phe Leu Asn Gly Ile
705 710 715 720

Asp Lys Ala Gln Glu Glu His Glu Lys Tyr His Ser Asn Trp Arg Ala
725 730 735

Met Ala Ser Asp Phe Asn Leu Pro Pro Val Val Ala Lys Glu Ile Val
740 745 750

Ala Ser Cys Asp Lys Cys Gln Leu Lys Gly Glu Ala Met His Gly Gln
755 760 765

Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr His Leu Glu
770 775 780

Gly Lys Ile Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu
785 790 795 800

Ala Glu Val Ile Pro Ala Glu Thr Gly Gln Glu Thr Ala Tyr Phe Leu
805 810 815

Leu Lys Leu Ala Gly Arg Trp Pro Val Lys Thr Ile His Thr Asp Asn
820 825 830

Gly Ser Asn Phe Thr Ser Thr Thr Val Lys Ala Ala Cys Trp Trp Ala
835 840 845

Gly Ile Lys Gln Glu Phe Gly Ile Pro Tyr Asn Pro Gln Ser Gln Gly
850 855 860

Val Val Glu Ser Met Asn Asn Glu Leu Lys Lys Ile Ile Gly Gln Val
865 870 875 880

Arg Asp Gln Ala Glu His Leu Lys Thr Ala Val Gln Met Ala Val Phe
885 890 895

Ile His Asn Phe Lys Arg Lys Gly Gly Ile Gly Gly Tyr Ser Ala Gly
900 905 910

Glu Arg Ile Val Asp Ile Ile Ala Thr Asp Ile Gln Thr Lys Glu Leu
915 920 925

Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Asp
12

930

935

940

Asn Lys Asp Pro Leu Trp Lys Gly Pro Ala Lys Leu Leu Trp Lys Gly
 945 950 955 960

Glu Gly Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val Val Pro
 965 970 975

Arg Arg Lys Ala Lys Ile Ile Arg Asp Tyr Gly Lys Gln Met Ala Gly
 980 985 990

Asp Asp Cys Val Ala Ser Arg Gln Asp Glu Asp
 995 1000

<210> 5
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(501)

<400> 5

atg aaa tat aca agt tat atc ttg gct ttt cag ctc tgc atc gtt ttg 48
 Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
 1 5 10 15

ggg tct ctt ggc tgt tac tgc cag gac cca tat gta aaa gaa gca gaa 96
 Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
 20 25 30

aac ctt aag aaa tat ttt aat gca ggt cat tca gat gta gcg gat aat 144
 Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
 35 40 45

gga act ctt ttc tta ggc att ttg aag aat tgg aaa gag gag agt gac 192
 Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
 50 55 60

aga aaa ata atg cag agc caa att gtc tcc ttt tac ttc aaa ctt ttt 240
 Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
 65 70 75 80

aaa aac ttt aaa gat gac cag agc atc caa aag agt gtg gag acc atc 288
 Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
 85 90 95

aag gaa gac atg aat gtc aag ttt ttc aat agc aac aaa aag aaa cga 336
 Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
 100 105 110

gat gac ttc gaa aag ctg act aat tat tcg gta act gac ttg aat gtc 384
 Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
 115 120 125

caa cgc aaa gca ata cat gaa ctc atc caa gtg atg gct gaa ctg tcg 432
 Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
 13

130	135	140	
cca gca gct aaa aca ggg aag cga aaa agg agt cag atg ctg ttt cga			480
Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg			
145	150	155	160

ggt cga aga gca tcc cag taa	501
Gly Arg Arg Ala Ser Gln	
	165

<210> 6
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145 150 155 160

Gly Arg Arg Ala Ser Gln
165

<210> 7
 <211> 11333

<212> DNA
 <213> recombinant vector

<400> 7
 agacagttat cccaatacgg tatacaagga gacaatttat caatttttgt agattcttcc 60
 aatgaagttg ctataaacag gcaactctatt ataggagcta gacagttgaa tcctatatgc 120
 gtagtatctt tttatccctt tgatccagaa cataaagttt ttttcgttat atatgttggt 180
 agatataaag ataagtattg tggaatttcc tacgtagctg atagagaaga tatgtacaaa 240
 gttatcaaca ggatataccc gtacgttagt tgtttttacc tcgtatcaga tgggtataata 300
 aattttcata ctactcccgt agctaatacac actagaaata ttaaaccctt tccagttaat 360
 tattgtaata ctttatgtga aatagtatat gattttgaat atttaaagtt tgaacaaggt 420
 gttatgtcta ttccgggtgt catgcctttt gtaccaaacc agtttgtatc tattatcaat 480
 ttaccagatg atattctcat aacatgtaca gcgtccagta acatagaata cataacacat 540
 atagataata aaaagctaaa aagaatactt ataataataa aagataaatt tctaaagggt 600
 actatcatgc aaggctactt taaaaaagta aatatcataa gacacaagaa gtatacatat 660
 actataacgt attcttcttt tgattgccct aaactagaag atactaagtc atcgctgcca 720
 agtacgtgca ataaagccat attagatggg cgtagatatg ttacaaaaac ttttaatgat 780
 acaatataaa tggaaatagc tagagaaacg ctaataacga taggccttac tatattagta 840
 gtgttattga taataactgg attctcgcta gtgctaagat taataccggg tgtttatagt 900
 tcagtatcga ggtcatcatt tacagcagga agaatacttc gttttatgga aatattttct 960
 actattatgt ttattcctgg aataattata ttgtacgctg cttatataag aaaaattaaa 1020
 atgaaaaata attagaatct gaaaatgtct tctggaagca tccatgttat tacaggccct 1080
 atgttttccg gtaaaacatc ggagctagta agaagaataa aaagatttat gctatctaac 1140
 tttaaatgta ttattattaa acattgtgga gataatagat ataatgagga tgatataaac 1200
 aaagtatata ctcatgatct attgtttatg gaggctacgg catcttctaa tctatctgta 1260
 ttagtaccta cgctattaaa tgatggagtt caggtaatag gtatagacga ggctcaattc 1320
 tttctagaca tagtagaatt tagtgaatcc atggctaatt taggtaaaac agttattgtg 1380
 gccgcgctta acggtgattt taaacgcgaa ttattcggta acgtatataa gttattatca 1440
 ttagctgaaa cagtgtccag ttgacagct atttgcgta aatgctattg cgacgcttcg 1500
 ttttctaaac gagttacaga aaataaagaa gtaatggata taggtggtaa agataaatac 1560
 atagccgtgt gtaggaaatg tttttttagt aattaagggg agatctcccc atggcccaaa 1620
 gcgggggttg aacagggttt cgctcaggtt tgcctgtgtc atggatgcag cctccagaat 1680
 acttactgga aactattgta acccgctga agttaaaaag aacaacgccc ggcagtgcca 1740
 ggcgttgaaa agattagcga ccggagattg gcgggacgaa tacgacgccc atatcccacg 1800

gctgttcaat	ccaggtatct	tgcgggatat	caacaacata	gtcatcaacc	agcggacgac	1860
cagccggttt	tgcaagatg	gtgacaaagt	gcgcttttgg	atacatttca	cgaatcgcaa	1920
ccgcagtacc	accggtatcc	accaggtcat	caataacgat	gaagccttcg	ccatcgctt	1980
ctgcgcgttt	cagcacttta	agctcgcgct	ggttgtcgtg	atcgtagctg	gaaatacaaa	2040
cggtatcgac	atgacgaata	cccagttcac	gcgccagtaa	cgcacccggt	accagaccgc	2100
cacggcttac	ggcaataatg	cctttccatt	gttcagaagg	catcagtcgg	cttgcgagtt	2160
tacgtgcatg	gatctgcaac	atgtcccagg	tgacgatgta	tttttcgctc	atgtgaagtg	2220
tcccagcctg	tttatctacg	gcttaaaaag	tgttcgaggg	gaaaataggt	tgcgcgagat	2280
tatagagatc	cgtcactgtt	ctttatgatc	tacttcctta	ccgtgcaata	aattagaata	2340
tattttctac	ttttacgaga	aattaattat	tgtattttatt	atttatgggt	gaaaaactta	2400
ctataaaaag	cgggtgggtt	tggaattagt	gatcagttta	tgtatatcgc	aactaccggc	2460
atatggctat	tcgacatcga	gaacattacc	cacatgataa	gagattgtat	cagtttcgta	2520
gtcttgagta	ttggtattac	tatatagtat	atgtcgggaa	ttcagatcca	tgcagatccc	2580
ccctgcccgg	ttattattat	ttttgacacc	agaccaactg	gtaatggtag	cgaccggcgc	2640
tcagctggaa	ttccgccgat	actgacgggc	tccaggagtc	gtcgccacca	atccccatat	2700
ggaaaccgtc	gatattcagc	catgtgcctt	cttccgcgtg	cagcagatgg	cgatggctgg	2760
tttccatcag	ttgctgttga	ctgtagcggc	tgatgttgaa	ctggaagtcg	ccgcgccact	2820
gggtgtgggcc	ataattcaat	tcgcgcgtcc	cgcagcgcag	accgttttcg	ctcggaaga	2880
cgtacgggggt	atacatgtct	gacaatggca	gatcccagcg	gtcaaaacag	gcggcagtaa	2940
ggcggtcggg	atagttttct	tgcggcccta	atccgagcca	gtttaccgcg	tctgctacct	3000
gcgccagctg	gcagttcagg	ccaatccgcg	ccggatgcgg	tgtatcgctc	gccacttcaa	3060
catcaacggt	aatcgccatt	tgaccactac	catcaatccg	gtaggttttc	cggctgataa	3120
ataaggtttt	cccctgatgc	tgccacgcgt	gagcggtcgt	aatcagcacc	gcatcagcaa	3180
gtgtatctgc	cgtgcactgc	aacaacgctg	cttcggcctg	gtaatggccc	gccgccttcc	3240
agcgttcgac	ccaggcggtta	gggtcaatgc	gggtcgcttc	acttacgcca	atgtcgttat	3300
ccagcgggtgc	acgggtgaac	tgatcgcgca	gcggcgtcag	cagttgtttt	ttatcgccaa	3360
tccacatctg	tgaaagaaag	cctgactggc	ggttaaattg	ccaacgctta	ttaccagct	3420
cgatgcaaaa	atccatttcg	ctggtgggtca	gatgcgggat	ggcgtgggac	gcggcgggga	3480
gcgtcacact	gaggttttcc	gccagacgcc	actgctgcca	ggcgtgatg	tgcccggctt	3540
ctgaccatgc	ggtcgcgttc	ggttgactta	cgcgtactgt	gagccagagt	tgcccggcgc	3600
tctccggctg	cggtagttca	ggcagttcaa	tcaactgttt	accttgtgga	gcgacatcca	3660
gaggcacttc	accgcttgcc	agcggcttac	catccagcgc	caccatccag	tgaggagct	3720

cgttatcgct atgacggaac aggtattcgc tggctacttc gatgggtttgc ccggataaac	3780
ggaactggaa aaactgctgc tgggtgttttg cttccgtcag cgctggatgc ggcgtagcgt	3840
cggcaaagac cagaccgttc atacagaact ggcgatcggt cggcgtagtc ccaaaatcac	3900
cgccgtaagc cgaccacggg ttgccgtttt catcatatct aatcagcgac tgatccaccc	3960
agtcccagac gaagccgccc tgtaaacggg gatactgacg aaacgcctgc cagtatttag	4020
cgaaaccgcc aagactgtta cccatcgctt gggcggtatt gcaaaggatc agcgggtagc	4080
tctctccagg tagcgaaagc cattttttga tggaccattt cggcacagcc ggggaagggt	4140
ggtcttcatc cacgtagcgc tacatcgggc aaataatctt ggtggcgtg gtgtcggctc	4200
cgccgccttc atactgcacc gggcggaag gatcgacaga ttgatccag cgatacagc	4260
cgctcgtgatt agcgcctggt cctgattcat tccccagcga ccagatgatc aactcgggt	4320
gattacgatc gcgctgcacc attcgcgtta cgcgttcgct catcgccgtt agccagcgc	4380
gatcatcgtt cagacgattc attggcacca tgccgtgggt ttcaatattg gcttcatcca	4440
ccacatacag gccgtagcgc tcgcacagcgc tgtaccacag cggatgggtt ggataatgc	4500
aacagcgcac ggcgttaaag ttgttctgct tcatcagcag gatatcctgc accatcgtct	4560
gctcatccat gacctgacca tgcagaggat gatgctcgtg acggttaacg cctcgaatca	4620
gcaacggctt gccgttcagc agcagcagac cattttcaat ccgcacctc cggaaaccga	4680
catcgcaggc ttctgcttca atcagcgtgc cgtcggcgtt gtgcagttca accaccgc	4740
gatagagatt cgggatttcg gcgctccaca gtttcgggtt ttcgacgttc agacgtagtg	4800
tgacgcgatc ggcataacca ccacgctcat cgataatttc accgccgaaa ggcgcggtgc	4860
cgctggcgac ctgcgtttca ccctgccata aagaaactgt taccgtagg tagtcacgca	4920
actcgcgcga catctgaact tcagcctcca gtacagcgcg gctgaaatca tcattaaagc	4980
gagtggcaac atggaaatcg ctgatttgtg tagtcgggtt atgcagcaac gagacgtcac	5040
ggaaaatgcc gctcatccgc cacatatcct gatcttccag ataactgccg tctctccaac	5100
gcagcaccat caccgcgagg cggttttctc cggcgcgtaa aaatgcgctc aggtcaaatt	5160
cagacggcaa acgactgtcc tggccgtaac cgaccacgcg cccgttgac cacagatgaa	5220
acgccgagtt aacgccatca aaaataattc gcgtctggcc ttctctgtagc cagctttcat	5280
caacattaaa tgtgagcgag taacaacccg tcggattctc cgtgggaaca aacggcggt	5340
tgaccgtaat gggataggtt acgttggtgt agatgggtagc atcgtaaccg tgcatctgcc	5400
agtttgaggg gacgacgaca gtatcggcct caggaagatc gactccagc cagctttccg	5460
gcaccgcttc tgggtgccga aaccaggcaa agcgcctatc gccattcagg ctgcgcaact	5520
gttgggaagg gcgatcgggt cgggcctctt cgctattacg ccagctggcg aaaggggat	5580
gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcacga cgttgtaaaa	5640

cgacgggatc tagcatggat ctagccat	ttt agtatcctaa aattgaattg taattatcga	5700
taataaatgg acggatcgat gaaatataca	agttatatct tggcttttca gctctgcatc	5760
gttttggtt ctcttggctg ttactgccag	gacccatatg taaaagaagc agaaaacctt	5820
aagaaatatt ttaatgcagg tcattcagat	gtagcggata atggaactct tttcttaggc	5880
atthtgaaga attggaaaga ggagagtgac	agaaaaataa tgcagagcca aattgtctcc	5940
ttttacttca aactttttta aaacttttaa	gatgaccaga gcatccaaaa gagtgtggag	6000
accatcaagg aagacatgaa tgtcaagttt	ttcaatagca acaaaaagaa acgagatgac	6060
ttcgaaaagc tgactaatta ttcggtaact	gacttgaatg tccaacgcaa agcaatacat	6120
gaactcatcc aagtgatggc tgaactgtcg	ccagcagcta aaacagggaa gcgaaaaagg	6180
agtcagatgc tgtttcgagg tcgaagagca	tcccagtaat ggttgtcctg cctgcaatat	6240
ttgaatttta aatctaaatc tatttattaa	tatttaacat tatttatatg gggaatatat	6300
ttttagactc atcaatcaaa taagtattta	taatagcaac ttttttgtaa tggatcccag	6360
ctctctcgac gcaggactcg gcttgctgaa	gcgcgcacag caagaggcga ggggcggcga	6420
ctggtgagta cgccaatttt tgactagcgg	aggctagaag gagagagaga tgggtgcgag	6480
agcgtcggta ttaagcgggg gagaattaga	taaatgggaa aaaattcggg taaggccagg	6540
gggaaagaaa aaatataagt taaaacatat	agtatgggca agcagggagc tagaacgatt	6600
cgcagtcaat cctggcctgt tagaaacatc	agaaggctgc agacaaatat tgggacagct	6660
acagccatcc cttcagacag gatcagaaga	acttagatca ttatataata cagtagcaac	6720
cctctattgt gtacatcaaa ggatagatgt	aaaagacacc aaggaagctt tagagaagat	6780
agaggaagag caaaacaaaa gtaagaaaaa	ggcacagcaa gcagcagctg cagctggcac	6840
aggaaacagc agccagggtca gccaaaatta	ccctatagtg cagaacctac aggggcaaat	6900
ggtacatcag gccatatcac ctagaacttt	aatgcatgg gtaaaagtag tagaagaaaa	6960
ggctttcagc ccagaagtaa taccatggtt	ttcagcatta tcagaaggag ccaccccaca	7020
agatttaaac accatgctaa acacagtggg	gggacatcaa gcagccatgc aaatgttaaa	7080
agagactatc aatgaggaag ctgcagaatg	ggatagagtgc catccagtgc atgcagggcc	7140
tattgcacca ggccaaatga gagaaccaag	gggaagtgac atagcaggaa ctactagtac	7200
ccttcaggaa caaataggat ggatgacaaa	taatccacct atcccagtag gagaaatcta	7260
taaaagatgg ataatcctgg gattaaataa	aatagtaaga atgtatagcc ctaccagcat	7320
tctggacata agacaaggac caaaggaacc	ctttagagat tatgtagacc ggttctataa	7380
aactctaaga gccgaacaag cttcacagga	tgtaaaaaat tggatgacag aaaccttggt	7440
ggtccaaaat gcaaaccagc attgtaagac	tatttttaaaa gcattgggac cagcagctac	7500
actagaagaa atgatgacag catgtcaggg	agtgggggga cccggccata aagcaagagt	7560

tttggctgaa	gccatgagcc	aagtaacaaa	tccagctaac	ataatgatgc	agagaggcaa	7620
tttttaggaac	caaagaaaga	ctgttaagtg	tttcaattgt	ggcaaagaag	ggcacatagc	7680
caaaaattgc	agggccccta	ggaaaaaggg	ctgttggaga	tgtggaaggg	aaggacacca	7740
aatgaaagat	tgcactgaga	gacaggctaa	tttttttaggg	aagatctggc	cttcctacaa	7800
gggaaggcca	gggaattttc	ttcagagcag	accagagcca	acagccccac	cagaagagag	7860
cttcaggttt	ggggaggaga	aaacaactcc	ctctcagaag	caggagccga	tagacaagga	7920
actgtatcct	ttaacttccc	tcagatcact	ctttggcaac	gacccctcgt	cacaataagg	7980
ataggggggc	aactaaagga	agctctatta	gatacaggag	cagatgatac	agtattagaa	8040
gaaatgaatt	tgccaggaaa	atggaaacca	aaaatgatag	ggggaattgg	aggttttatc	8100
aaagtaagac	agtacgatca	gatacctgta	gaaatctgtg	gacataaagc	tataggtaca	8160
gtattagtag	gacctacacc	tgtcaacata	attggaagaa	atctgttgac	tcagattggt	8220
tgtactttta	atttccccat	tagtcctatt	gaaactgtac	cagtaaaatt	aaagccagga	8280
atggatggcc	caaaagttaa	gcaatggcca	ttgacagaag	aaaaaataaa	agcattagta	8340
gagatatgta	cagaaatgga	aaaggaaggg	aaaatttcaa	aaattgggcc	tgaaaatcca	8400
tacaatactc	cagtatttgc	tataaagaaa	aaagacagta	ctaaatggag	aaaactagta	8460
gatttcagag	aacttaataa	aagaactcaa	gacttctggg	aagttcagtt	aggaatacca	8520
caccccgag	ggttaaaaaa	gaaaaaatca	gtaacagtat	tggatgtggg	tgatgcatac	8580
ttttcagttc	ccttagataa	agactttaga	aagtatactg	cattttaccat	acctagtata	8640
aacaatgaga	caccagggat	tagatatcag	tacaatgtgc	tgccacaggg	atggaaagga	8700
tcaccagcaa	tattccaaag	tagcatgaca	aaaatccttag	agccttttag	aaaacagaat	8760
ccagacatag	ttatctatca	atacatggat	gatttgtatg	taggatctga	cttagaaata	8820
gggcagcata	gaacaaaaat	agaggaactg	agacagcatc	tgttgaggtg	gggatttacc	8880
acaccagaca	aaaaacatca	gaaagaacct	ccatttccttt	ggatgggtta	tgaactccat	8940
cctgataaat	ggacagtaca	gcctataatg	ctgccagaaa	aagacagctg	gactgtcaat	9000
gacatacaga	agttagtggg	aaaattgaat	tgggcaagtc	agatttatgc	agggattaaa	9060
gtaaagcagt	tatgtaaact	ccttagagga	accaaagcac	taacagaagt	aataccacta	9120
acagaagaag	cagagctaga	actggcagaa	aacagggaga	ttctaaaaga	accagtacat	9180
gaagtatatt	atgacctatc	aaaagactta	gtagcagaaa	tacagaagca	ggggcaaggc	9240
caatggacat	atcaaattta	tcaagagcca	tttaaaaatc	tgaaaacagg	aaagtatgca	9300
aggatgaggg	gtgcccacac	taatgatgta	aaacagttta	cagaggcagt	gcaaaaagta	9360
tccacagaaa	gcatagtaat	atggggaaag	attcctaaat	ttaaactacc	catacaaaag	9420
gaaacatggg	aagcatggtg	gatggagtat	tggcaagcta	cctggattcc	tgagtgggag	9480

tttgtcaata	ccccctccctt	agtgaaatta	tggtaccagt	tagagaaaga	acccatagta	9540
ggagcagaaa	ctttctatgt	agatggggca	gctaataggg	agactaaatt	aggaaaagca	9600
ggatatgtta	ctgacagagg	aagacaaaaa	gttgtctcca	tagctgacac	aacaaatcag	9660
aagactgaat	tacaagcaat	tcatctagct	ttgcaggatt	cgggattaga	agtaaacata	9720
gtaacagact	cacaatatgc	attaggaatc	attcaagcac	aaccagataa	gagtgaatca	9780
gagttagtca	gtcaaataat	agagcagtta	ataaaaaagg	aaaagggtcta	cctggcatgg	9840
gtaccagcac	acaaaggaat	tggaggaaat	gaacaagtag	ataaattagt	cagtgtctgga	9900
atcaggaaaag	tactatTTTT	gaatggaata	gataaggccc	aagaagaaca	tgagaaatat	9960
cacagtaatt	ggagagcaat	ggctagtgat	tttaacctgc	cacctgtagt	agcaaaagaa	10020
atagtagcca	gctgtgataa	atgtcagcta	aaaggagaag	ccatgcatgg	acaagtagac	10080
tgtagtccag	gaatatggca	actagattgt	acacatctag	aaggaaaaat	tatcctggta	10140
gcagttcatg	tagccagtgg	atatatagaa	gcagaagtta	ttccagcaga	gacagggcag	10200
gaaacagcat	attttctctt	aaaatttagca	ggaagatggc	cagtaaaaac	aatacataca	10260
gacaatggca	gcaatttcac	cagtactacg	gttaaggccg	cctgttggtg	ggcagggatc	10320
aagcaggaat	ttggcattcc	ctacaatccc	caaagtcaag	gagtagtaga	atctatgaat	10380
aatgaattaa	agaaaattat	aggacaggta	agagatcagg	ctgaacacct	taagacagca	10440
gtacaaatgg	cagtattcat	ccacaatttt	aaaagaaaag	gggggatttg	gggatacagt	10500
gcaggggaaa	gaatagtaga	cataatagca	acagacatac	aaactaaaga	actacaaaag	10560
caaattacaa	aaattcaaaa	ttttcggggt	tattacaggg	acaacaaaga	tccccttttg	10620
aaaggaccag	caaagcttct	ctggaaaggt	gaaggggcag	tagtaataca	agataatagt	10680
gacataaaaag	tagtgccaag	aagaaaagca	aaaatcatta	gggattatgg	aaaacagatg	10740
gcaggtgatg	attgtgtggc	aagtagacag	gatgaggatt	agaacatgga	aaagtttagt	10800
aaaacaccat	agggtcgact	gcagaagctt	ccatggggag	ctcttttagtg	taataaattt	10860
aataaaatat	tgacaaaata	gttaaataaa	tatatgaaag	tacattatac	acggaatgga	10920
gttcgatatt	agttcttgca	gaatgatata	ttctgttctc	gaacaatatc	actttgttac	10980
tgataatcgt	tataacaacc	ataatcaaaa	atttagaatt	atattatact	gtttaaaaga	11040
ttctacgata	aagaaatatc	cgtacagggt	tgtttctgaa	attcactttg	taagatacat	11100
aattaacaaa	ttcaggggga	aaaatcttta	caaaattagt	atagaagcta	tagatatatc	11160
aaaaggtaga	caacaaataa	tcagaacctt	atttttttat	caaaaaatta	aaatataaat	11220
aaaatgaaaa	ataacttgta	tgaagaaaaa	atgaacatga	gtaagaaaca	agtaaaaact	11280
caaagtaaat	gtaataataa	cgcactctaga	tttcatgcc	tggatgcggt	gca	11333